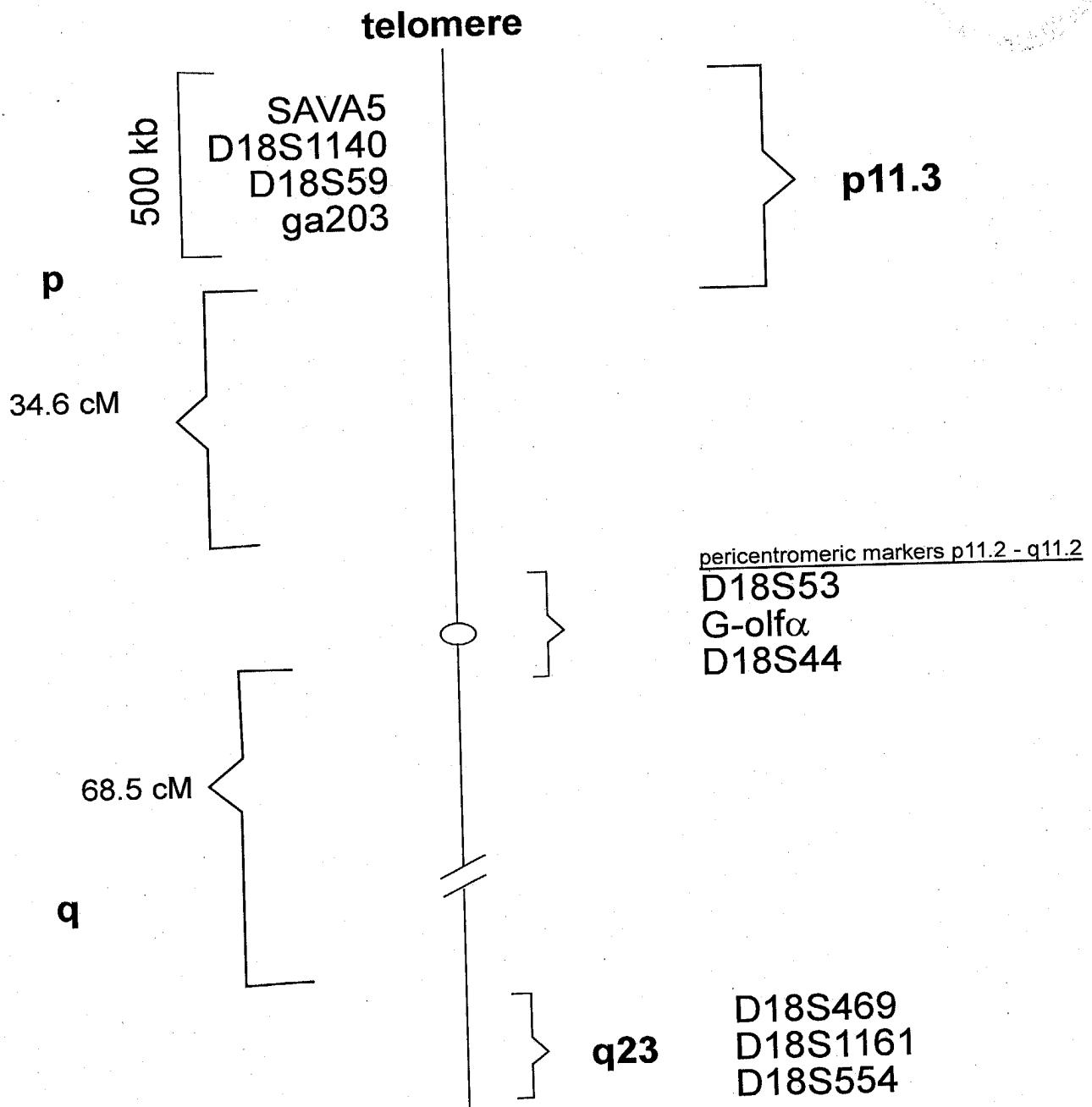


EXHIBIT 1
08/976,560



Lod scores for markers exceeding the arbitrary coverage thresholds.

Marker Name	distance from pter	Family CR001		Family CR004		Combined	
		Z _{max} ≥ 0.8	Theta	Z _{max} ≥ 1.2	Theta	Z _{max} ≥ 1.6	Theta
<i>D1S456</i>	224.6	1.32	0.0	0.0	0.50	0.0	0.50
<i>D2S130</i>	230.1	0.89	0.0	0.12	0.35	0.36	0.26
<i>D3S1285</i>	91.0	0.00	0.50	2.59	0.00	1.13	0.16
<i>D4S171</i>	207.9	1.07	0.07	0.01	0.05	0.22	0.29
<i>D5S427</i>	69.6	1.39	0.0	0.0	0.50	0.7	0.18
<i>D7S510</i>	60.5	0.04	0.40	2.04	0.0	0.82	0.17
<i>D11S929</i>	36.3	0.80	0.11	0.03	0.42	0.43	0.24
<i>D11S1392</i>	38.6	0.86	0.07	0.90	0.23	1.58	0.19
<i>D11S1312</i>	42.0	0.47	0.13	1.77	0.0	1.95	0.05
<i>D13S175</i>	7.4	0.83	0.0	0.0	0.50	0.24	0.15
<i>D15S126</i>	45.5	1.09	0.0	0.0	0.48	0.06	0.40
<i>D16S521</i>	4.6	1.46	0.0	0.41	0.26	1.18	0.17
<i>D16S515</i>	94.8	0.93	0.09	0.01	0.46	0.39	0.25
<i>D16S486</i>	133.6	0.27	0.19	1.29	0.20	1.60	0.20
<i>D17S849</i>	0.60	0.0	0.50	1.22	0.07	0.32	0.14
<i>D18S59</i>	1.1	1.43	0.0	0.0	0.50	0.02	0.46
<i>D18S1105</i>	2.8	0.97	0.0	0.01	0.47	0.01	0.46
<i>D18S71</i>	43.8	0.96	0.0	0.0	0.50	0.0	0.50
<i>D18S64</i>	84.0	0.33	0.11	1.34	0.15	1.67	0.13
<i>D18S55</i>	95.5	0.0	0.50	2.09	0.13	1.51	0.18
<i>D18S61</i>	103.8	0.0	0.50	2.26	0.12	1.94	0.16
<i>D18S488</i>	105.6	0.0	0.50	1.26	0.14	1.02	0.19
<i>D18S1161</i>	113.0	0.0	0.50	1.79	0.16	1.76	0.17

Markers for which lod scores exceeded the arbitrary thresholds used for genome coverage calculations (in bold). Z_{max} is the maximum likelihood estimate of the lod score at the corresponding value of the recombination fraction (theta).

Figure 2